

a. constructing a multiple alignment of at least two amino acid sequences known to have three-dimensional structures similar to endoglucanase V (EGV) from *Humicola insolens* known from Protein Data Bank entry 4ENG;

- b. constructing a homology-built three-dimensional structure of the cellulolytic enzyme based on the structure of the EGV;
- c. identifying amino acid residue positions present in a distance from the substrate binding cleft of not more than 5Å;
- d. identifying surface-exposed amino acid residues of the enzyme;
- e. identifying all charged or potentially charged amino acid residue positions of the enzyme;
- f. choosing one or more positions wherein the amino acid residue is to be substituted, deleted or where an insertion is to be provided; and
- g. carrying out the substitution, deletion or insertion by using conventional protein engineering techniques. Also described are cellulase variants obtained by this method.